

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.  
Goli, Surya K.

(ii) TITLE OF THE INVENTION: HUMAN LEA-MOTIF DEVELOPMENTAL PROTEIN

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Filed Herewith  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER: PF-0213 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555  
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Val Lys Tyr Phe Leu Gly Gln Ser Val Leu Arg Ser Ser Trp Asp  
1 5 10 15  
Gln Val Phe Ala Ala Phe Trp Gln Arg Tyr Pro Asn Pro Tyr Ser Lys  
20 25 30

His Val Leu Thr Glu Asp Ile Val His Arg Glu Val Thr Pro Asp Gln  
     35                  40                  45  
 Lys Leu Leu Ser Arg Arg Leu Leu Thr Lys Thr Asn Arg Met Pro Arg  
     50                  55                  60  
 Trp Ala Glu Arg Leu Phe Pro Ala Asn Val Ala His Ser Val Tyr Val  
     65                  70                  75                  80  
 Leu Glu Asp Ser Ile Val Asp Pro Gln Asn Gln Thr Met Thr Phe  
     85                  90                  95  
 Thr Trp Asn Ile Asn His Ala Arg Leu Met Val Val Glu Glu Arg Cys  
     100                 105                 110  
 Val Tyr Cys Val Asn Ser Asp Asn Ser Gly Trp Thr Glu Ile Arg Arg  
     115                 120                 125  
 Glu Ala Trp Val Ser Ser Ser Leu Phe Gly Val Ser Arg Ala Val Gln  
     130                 135                 140  
 Glu Phe Gly Leu Ala Arg Phe Lys Ser Asn Val Thr Lys Thr Met Lys  
     145                 150                 155                 160  
 Gly Phe Glu Tyr Ile Leu Ala Lys Leu Gln Gly Glu Ala Pro Ser Lys  
     165                 170                 175  
 Thr Leu Val Glu Thr Ala Lys Glu Ala Lys Glu Lys Ala Lys Glu Thr  
     180                 185                 190  
 Ala Leu Ala Ala Thr Glu Lys Ala Lys Asp Leu Ala Ser Lys Ala Ala  
     195                 200                 205  
 Thr Lys Lys Gln Gln Gln Gln Gln Phe Val  
     210                 215

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 858 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GC GG TG GT GA	CT GAG CT ACG	AG C CT GG CG	C GG GT GT GC	CC G AG C C C C G	G C C C G G C C C G	60
G C C C T C G C T	G C C T C C C A G G	C T C C G C A C C C	C T G AT G C T G C	G C G G G T G C T G	A G C C C G C T T C	120
G G C C G G G A C G	A T G G T G A A G T	A T T T C C T G G G	C C A G A G C G T G	C T C C G G A G T T	C C T G G G A C C A	180
A G T G T T C G C C	G C C T T C T G G C	A G C G G T A C C C	G A A T C C C T A T	A G C A A A C A T G	T C T T G A C G G A	240
A G A C A T A G T A	C A C C G G G A G G	T G A C C C T G A	C C A G A A A C T G	C T G T C C C G G C	G A C T C C T G A C	300
C A A G A C C A A C	A G G A T G C C A C	G C T G G G C C G A	G C G A C T A T T T	C C T G C C A A T G	T T G C T C A C T C	360
G G T G T A C G T C	C T G G A G G A C T	C T A T T G G G A	C C C A C A G A A T	C A G A C C A T G A	C T A C C T T C A C	420
C T G G A A C A T C	A C C A C G C C C	G G C T G A T G G T	G G T G G A G G A A	C G A T G T G T T T	A C T G T G T G A A	480
C T C T G A C A A C	A G T G G C T G G A	C T G A A A T C C G	C C G G G A A G C C	T G G G T C T C C T	C T A G C T T A T T	540
T G G T G T C T C C	A G A G C T G T C C	A G G A A T T T G G	T C T T G C C C G G	T T C A A A A G C A	A C G T G A C C A A	600
G A C T A T G A A G	G G T T T T G A A T	A T A T C T T G G C	T A A G C T G C A A	G G C G A G G C C C	C T T C C A A A A C	660
A C T T G T T G A G	A C A G C C A A G G	A A G C C A A G G A	G A A G G C A A A G	G A G A C G G C A C	T G G C A G C T A C	720
A G A G A A G G C C	A A G G A C C T C G	C C A G C A A G G C	G G C C A C C A A G	A A G C A G C A G C	A G C A G C A A C A	780
G T T T G T G T A G	C C A G T C T A C C	A C C A C C A C A G	C A C C C C A G A C	A G C T A G G C T T	A G C C C C T C T G	840
C C C T C C C T T C	A T T G T A C T					858

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 215 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank  
(B) CLONE: 969170

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Lys Tyr Cys Ala Ser Leu Gly Val Leu Lys Gly Pro Trp Asp  
1 5 10 15  
Gln Val Phe Ala Ala Phe Trp Gln Arg Tyr Pro Asn Pro Tyr Ser Lys  
20 25 30  
His Val Leu Thr Glu Asp Ile Val His Arg Glu Val Thr Ala Asp His  
35 40 45  
Lys Leu Leu Ser Arg Arg Leu Leu Thr Lys Thr Asn Arg Met Pro Arg  
50 55 60  
Trp Ala Glu Arg Phe Phe Pro Ala Asn Val Ala His Asn Val Tyr Ile  
65 70 75 80  
Val Glu Asp Ser Ile Val Asp Pro Lys Asn Arg Thr Met Thr Phe  
85 90 95  
Thr Trp Asn Ile Asn His Ala Arg Leu Met Ala Val Glu Glu Arg Cys  
100 105 110  
Val Tyr Arg Val Asn Pro Glu Asn Ser Ser Trp Thr Glu Val Lys Arg  
115 120 125  
Glu Ala Trp Val Ser Ser Ser Leu Phe Gly Val Ser Arg Ala Val Gln  
130 135 140  
Glu Phe Gly Leu Ala Arg Phe Lys Ser Asn Val Thr Lys Ser Thr Lys  
145 150 155 160  
Gly Phe Glu Tyr Val Leu Ala Arg Met Gln Gly Glu Ala Pro Ser Lys  
165 170 175  
Thr Leu Val Glu Thr Ala Lys Glu Ala Thr Glu Lys Ala Lys Glu Thr  
180 185 190  
Ala Leu Ala Ala Thr Glu Lys Ala Lys Asp Leu Ala Ser Lys Ala Ala  
195 200 205  
Thr Lys Lys Lys Gln Phe Val  
210 215